

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 ; Search time 9.41818 Seconds
(without alignments)
1225.145 Million cell updates/sec

Title: US-09-988-971-2_COPY_35_90
Perfect score: 288
Sequence: 1 ATAAVAGSEFPAGPAELSLR.....VLSEVSGREYINIPSHVAVK 56

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	288	100.0	210 4	Q8WY18
2	288	100.0	261 4	Q8H6Q3
3	242	84.0	259 11	Q8V142
4	242	84.0	259 11	Q8R4L0
5	143	49.7	197 4	Q9H135
6	140	48.6	63 4	Q96Q14
7	109.5	38.0	517 5	Q77050
8	100	34.7	505 4	Q96IN1
9	99	34.4	161 4	Q9HBI7
10	99	34.4	276 4	Q13239
11	97	33.7	280 11	Q8QZX8
12	97	33.7	281 11	Q8Q898
13	95.5	33.2	527 5	Q9Y121
14	93	32.3	511 5	Q8WQMS
15	91.5	31.8	517 5	Q9V9J3
16	90	31.2	121 4	Q9H4Y2

17	90	31.2	502 13	Q9DDK6	Q94dk6 salmo salar
18	88	30.6	509 6	Q95M32	Q95m32 hylobates s
19	88	30.6	509 11	Q91X65	Q91x65 mus musculus
20	87.5	30.4	153 13	Q91E78	Q91e78 brachydontio
21	87.5	30.4	193 13	Q90993	Q90993 gallus gall
22	87.5	30.4	204 15	Q85730	Q85730 rous sarcom
23	87.5	30.4	285 15	Q85476	Q85476 rous sarcom
24	87.5	30.4	526 15	Q60567	Q60567 rous sarcom
25	87.5	30.4	526 15	Q92806	Q92806 rous sarcom
26	87.5	30.4	587 15	Q64817	Q64817 avian sarco
27	87	30.2	488 13	Q13064	Q13064 xenopus lae
28	87	30.2	509 6	Q95K87	Q95k87 saimiri sci
29	85	29.5	1049 5	Q00851	Q00851 entamoeba h
30	84.5	29.3	495 5	Q8MSU4	Q8msu4 ephydactia f
31	84.5	29.3	541 11	Q99PW1	Q99pw1 rattus norv
32	83.5	29.0	527 13	Q91952	Q91952 xiphophorus
33	83.5	29.0	534 4	Q16248	Q16248 homo sapien
34	83.5	29.0	534 4	Q95M31	Q95m31 hylobates s
35	82.5	28.6	504 5	Q8WSU2	Q8wsu2 ephydactia f
36	82.5	28.6	542 11	Q9UJ10	Q9uj10 rattus norv
37	82.5	28.6	682 5	Q25432	Q25432 lyechinus
38	82.5	28.6	496 13	Q93411	Q93411 xenopus lae
39	82	28.5	523 15	Q85477	Q85477 rous sarcom
40	81.5	28.3	526 15	Q64993	Q64993 rous sarcom
41	81.5	28.3	526 15	Q64994	Q64994 rous sarcom
42	81.5	28.3	526 15	Q93080	Q93080 rous sarcom
43	81.5	28.3	535 15	Q92957	Q92957 rous sarcom
44	81.5	28.3	545 15	Q86362	Q86362 rous sarcom
45	81.5	28.3			

ALIGNMENTS

RESULT 1
Q8WY18 PRELIMINARY; PRT; 210 AA.

AC Q8WY18; 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Modulator of antigen receptor signaling, putative splice isoform
DE WARS-V.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMUS;
RA Loreto W.P., McGlade C.J.;
RT "Modulator of Antigen Receptor Signaling (WARS) - putative splice variant.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF290986; AAL38198.1; -
DR InterPro; IPR000980; SH2
DR InterPro; IPR001452; SH2
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH2; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH2DOMAIN.
DR PRODOM; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PSS0001; SH2; 1.
DR PROSITE; PSS0002; SH3; 1.
KW RECEPTOR.
SQ SEQUENCE 210 AA; 23103 MW; BED62208E53A472E CRC64;

Query Match 100.0%; Score 288; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 4.5e-27;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 56
 DB 35 ATVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 90

RESULT 2

Q9H6Q3 PRELIMINARY; PRT; 261 AA.

AC Q9H6Q3;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE CDNA: FLN21992.F18, clone HEP06554 (Src-like adapter protein-2)
 DE (Modulator of antigen receptor signaling MARS).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawabata A., Hiki J., Kobayake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isozaki T., Sugano S.,
 RT "NEBO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21553259; PubMed=11696592;
 RA Holland S.J., Liao X.C., Mendenhall M.K., Zhou X., Pardo J., Chu P.,
 RA Spencer C., Fu A.C., Sheng N., Yu P., Pali E., Negin A., Shen M.,
 RA Yu S., Chan E., Wu X., Li C., Weisenschlager M., Averis G.,
 RA Kolbinger F., Bennett M.K., Moliniaux S., Luo Y., Payan D.G.,
 RA Manabeo H.S.Y., Wu J.;
 RT "Functional Cloning of Src-like Adapter Protein-2 (SLAP-2), a Novel
 RT Inhibitor of Antigen Receptor Signaling."
 RL J. Exp. Med. 194:1263-1276(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYMUS;
 RA Loreto M.P., McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS)."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: AK025645; BAB15201.1; -;
 DR EMBL: AF236353; AAL29204.1; -;
 DR EMBL: AF230985; AAL38197.1; -;
 DR HSSP: P06239; ILK.
 DR InterPro: IPR000960; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW SH3 domain; Receptor.

QY SEQUENCE 261 AA; 28585 MW; 858AF0345167B3D CRC64;

Query Match 100.0%; Score 288; DB 4; Length 261;
 Best Local Similarity 100.0%; Pred. No. 5,8e-27;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 56
 DB 35 ATVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 90

RESULT 3

Q8V142 PRELIMINARY; PRT; 259 AA.

DT 01-MAR-2002 (TRENBLrel. 20, Created)
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Modulator of antigen receptor signaling MARS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loreto M.P., McGlade C.J.;
 RT "Modulator of Antigen Receptor Signaling (MARS)."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF287467; AAL38196.1; -;
 DR InterPro: IPR000960; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Receptor.
 QY SEQUENCE 259 AA; 28476 MW; 8270F17CD3FC50A3 CRC64;

Query Match 84.0%; Score 242; DB 11; Length 259;
 Best Local Similarity 85.5%; Pred. No. 2,2e-21;
 Matches 47; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TAVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 56
 DB 35 TAVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 89

RESULT 4

Q8R4L0 PRELIMINARY; PRT; 259 AA.

DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Src-like adapter protein-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pandey A., Ibarrol N., Kratchmarova I., Fernandez M.,
 RA Constantinescu S., Ohara O., Sawasdi Kosol S., Lodish H.F., Mann M.;
 RT "A novel Src homology 2 domain-containing molecule, Src-like Adapter
 RT Protein-2 (SLAP-2), which negatively regulates T cell receptor
 RT signaling."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ibarrola N., Mann M., Pandey A.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF434990; AAL86403.1; -;
 QY SEQUENCE 259 AA; 28516 MW; 1388E68244152E34 CRC64;

Query Match 84.0%; Score 242; DB 11; Length 259;
 Best Local Similarity 85.5%; Pred. No. 2,2e-21;
 Matches 47; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TAVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 56
 DB 35 TAVALGSPAGGPAELSLRLGEPPLTIVSDDGDMWTVLSEVSGREYNIPSVYAV 89

RESULT 5.

Q9H135 PRELIMINARY; PRT; 197 AA.
 AC Q9H135; 09H135; 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE D3977B1.1 (Novel protein tyrosine kinase with Src homology domain 2 (SH2) domains) (Fragment).
 GN D3977B1.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lloyd D.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050318; CAB75365.1; -.
 DR HSSP; P06239; ILKK.
 DR InterPro; IPR000980; SH2.
 DR Pfam; PF00017; SH2; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 KW Kinase.
 FT NON TER 1
 SQ SEQUENCE 197 AA; 22124 MW; EF01FE7A85C5C1F1 CRC64;

Query Match

Best Local Similarity 49.7%; Score 143; DB 4; Length 197;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 DGDWTVLSEVSGREYNIPSVHAKV 56
 DB 1 DGDWTVLSEVSGREYNIPSVHAKV 26

RESULT 6

Q96Q14 PRELIMINARY; PRT; 63 AA.
 AC Q96Q14; 096Q14; 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE D36098.2 (Novel protein tyrosine kinase with Src homology 2 (SH2) domain) (Fragment).
 GN D3977B1.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Skuce C.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031662; CAC44645.1; -.
 KW Kinase.
 FT NON TER 63
 SQ SEQUENCE 63 AA; 6350 MW; 3EC599C9F1723053 CRC64;

Query Match 48.6%; Score 140; DB 4; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAAAGSPAGAPALSLRIGEPPLTVS 29
 DB 35 ATAAAGSPAGAPALSLRIGEPPLTVS 63

RESULT 7

077050

ID 077050 PRELIMINARY; PRT; 517 AA.
 AC 077050; 077050; 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DE Src-type protein tyrosine kinase.
 GN ACSRC1.
 OS Anthocidaris crassispina (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidae; Euechinoidae; Echinacea; Echinoidae; Echinometridae; Anthocidaris.
 OX NCBI_TaxId=7629;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Onodera H., Kobari K., Sakuma M., Sato M., Suyemitsu T., Yamasu K.;
 RT "Expression of a src-type protein tyrosine kinase gene, Acsrc1, in the sea urchin embryo.";
 RL Dev. Growth Differ. 0:0-0(1999).
 CC EMBL; AB016815; BAA33741.1; -.
 DR HSSP; P00523; 2PTK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR ATP-binding; Kinase; SH3 domain; Transferase; Tyrosine-protein kinase.
 KW
 FT
 SQ SEQUENCE 517 AA; 58568 MW; D249A3DC35E3CA1 CRC64;

Query Match

Best Local Similarity 38.0%; Score 109.5; DB 5; Length 517;
 Matches 24; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

QY 2 TAAVAGSPAGAPALSLRIGEPPLTVS-DGDWTVLSEVSGREYNIPSVHAKV 56
 DB 68 TAAVAGSPAGAPALSLRIGEPPLTVS-DGDWTVLSEVSGREYNIPSVHAKV 123

RESULT 8

Q96IN1 PRELIMINARY; PRT; 505 AA.
 AC Q96IN1; 096IN1; 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Unknown (protein for MGC:16168).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007371; AA07371.1; -.
 DR InterPro; IPR000719; Euk_pkinase.

DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF000069; Pkinase; 1.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 505 AA; 57706 MW; B5F739BEF8389176 CRC64;

Query Match 34.7%; Score 100; DB 4; Length 505;
 Best Local Similarity 41.5%; Pred. No. 0.000911;
 Matches 22; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

QY 4 VALGSPAGPAELSLRLGEPPLTVSEEDGDMWTVLSEVSGREYNIPSYHAKV 56
 DB 64 VALVYTYMNRDQLQMLKGEKLVKGTGDMWLARSLVYRGSGVPSNFARV 116

RESULT 9
 Q9HB17 PRELIMINARY; PRT; 161 AA.

AC Q9HB17; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Src-1-like adapter protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonge, Rd., Schilhabel M.B., Menzel U., Detle M.D., Baumgart C.,
 RA Jahn N., Rosenthal A.;
 RT "Chromosome 8 genomic sequence";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Genome Sequencing Center Jena;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; AF235100; AAC29878.1; -.
 DR HSPF; P08631; 3HCK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW SH3 domain.
 FT NON TER 161
 SQ SEQUENCE 161 AA; 18493 MW; FC2854668045B20 CRC64;

Query Match 34.4%; Score 99; DB 4; Length 161;
 Best Local Similarity 37.3%; Pred. No. 0.0003;
 Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 6 LGSPAGPAELSLRLGEPPLTVSEEDGDMWTVLSEVSGREYNIPSYHAKV 56
 DB 30 LSDYSPDISPPIFRGKELRVISDEGGMWKAISLTGRESYIPGICVARV 80

RESULT 10
 Q13239 PRELIMINARY; PRT; 276 AA.

AC Q13239; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Putative SRC-1-like adapter protein (SLAP) (SRC-1-like-adapter).
 GN SLAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96423054; PubMed=8825655;
 RA Anglist M., Wells D.E., Chakravarti A., Pandey A.;
 RT "Chromosomal localization of the mouse Src-1-like adapter protein (Slap) gene and its putative human homolog SLA";
 RL Genomics 30:623-625 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Meljertink P.H.S., Zorn G., Bicker H., Bolhuis P.A., Baas F.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ohtsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,
 RA Miura Y.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,
 RA Jonge, Rd., Schilhabel M., Men G., Menzel U., Detle M., Baumgart C.,
 RA Rosenthal A.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BONE MARROW;
 RA Strussberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL; U30473; AAC50357.1; -.
 DR EMBL; U44403; AAC27662.1; -.
 DR EMBL; D89077; BA13758.1; -.
 DR EMBL; AF305872; BA137933.1; -.
 DR EMBL; BC007042; AA07042.1; -.
 DR HSPF; P08631; 3HCK.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW SH3 domain.
 FT NON TER 276
 SQ SEQUENCE 276 AA; 31156 MW; B0FC7D7B2ECA378 CRC64;

Query Match 34.4%; Score 99; DB 4; Length 276;
 Best Local Similarity 37.3%; Pred. No. 0.00056;
 Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 6 LGSPAGPAELSLRLGEPPLTVSEEDGDMWTVLSEVSGREYNIPSYHAKV 56
 DB 30 LSDYSPDISPPIFRGKELRVISDEGGMWKAISLTGRESYIPGICVARV 80

RESULT 11
 Q8QZ8 PRELIMINARY; PRT; 280 AA.

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AC 0806A8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Src-like adapter protein SLAP (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, AND ISS;
RX MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
Beeson M., Gordon L., Bennett B., Johnson T.B., Sikele J.M.;
RT "High-throughput sequence identification of gene coding variants
within alcohol-related Orls.";
RL Mamm. Genome 12:657-663(2001).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=ILS, AND ISS;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
Beeson M., Gordon L., Bennett B., Johnson T.B., Sikele J.M.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY079449; AL87537.1; -
DR EMBL: AY079450; AL87538.1; -
FT NON_TER
FT 1
SQ SEQUENCE 280 AA; 31549 MW; A05C3BF7FEAD951 CRC64;

Query Match 33.7%; Score 97; DB 11; Length 280;
Best Local Similarity 37.3%; Pred. No. 0.001;
Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 6 LGSFPAAGPAELSLRLEPPTIVSESGDMWTVLSEVSGREYNIPSHVAVY 56
Db 29 LIDYSPDISPPIFRREGKRLVISEDGGMWKAISLSTGRSYPICVAVY 79

RESULT 12
ID 060898 PRELIMINARY; PRT; 281 AA.
AC 060898;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE SRC-like adapter protein.
GN SLA OR SLAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95370243; PubMed=7543898;
RA Pandey A., Duan H., Dixit V.M.;
RT "Characterization of a novel Src-like adapter protein that associates
with the Eck receptor tyrosine kinase.";
RL J. Biol. Chem. 270:19201-19204(1995).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093985; PubMed=10630289;
RA Carrier A., Nguyen C., Vitorero G., Granjeaud S., Rocha D.,
Bernard K., Mlasek A., Ferrier P., Malsien M., Naquet P.,
Malsien B., Jordan B.;
RT "Differential gene expression in CD3e- and RAG1-deficient thymuses:
RT definition of a set of genes potentially involved in thymocyte
maturation.";
RL Immunogenetics 50:255-270(1999).
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL: U29056; AAA82756.1; -
DR EMBL: AJ131777; CAB66139.1; -
DR HSSP; P16277; 1BLK.

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DR MGD; MGI:104295; SLA.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR KX SH3 domain.
SQ SEQUENCE 281 AA; 31680 MW; B347921656A7ADA1 CRC64;

Query Match 33.7%; Score 97; DB 11; Length 281;
Best Local Similarity 37.3%; Pred. No. 0.001;
Matches 19; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

Qy 6 LGSFPAAGPAELSLRLEPPTIVSESGDMWTVLSEVSGREYNIPSHVAVY 56
Db 30 LIDYSPDISPPIFRREGKRLVISEDGGMWKAISLSTGRSYPICVAVY 80

RESULT 13
ID 09Y1Z1 PRELIMINARY; PRT; 527 AA.
AC 09Y1Z1;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Protein tyrosine kinase.
GN EPTK3 OR EPTK2.
OS Ephydaria fluvialilis.
OC Eukaryota; Metazoa; Porifera; Demosporiidae; Ctenophora;
Haplocleridae; Spongiillidae; Ephydaria.
OX NCBI_TaxId=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99246375; PubMed=10229568;
RA Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
Miyata T.;
RT "Extensive gene duplication in the early evolution of animals before
the parazoan-eumetazoan split demonstrated by G proteins and protein
tyrosine kinases from sponge and hydra.";
RL J. Mol. Evol. 48:646-653(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21601119; PubMed=11738833;
RA Suga H., Katoh K., Miyata T.;
RT "Sponge homologs of vertebrate protein tyrosine kinases and frequent
domain shufflings in the early evolution of animals before the
parazoan-eumetazoan split.";
RL Gene 280:195-201(2001).
DR EMBL; AB006557; BAA81711.2; -
DR EMBL; AB049592; BAB82421.1; -
DR HSSP; P11362; 1FGK.
DR InterPro; IPR000719; Euk_kinase.
DR InterPro; IPR002280; Set_cmr_kinase.
DR InterPro; IPR000960; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; pkkinase; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00220; S_TKc; 1.

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DR SMART: SM00219; TykC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW KINASE
 SEQUENCE 527 AA; 58101 MW; FEIEIEA836DF5C39 CRC64;

Query Match 33.2%; Score 95.5; DB 5; Length 527;
 Best Local Similarity 42.6%; Pred. No. 0.0034;
 Matches 23; Conservative 9; Mismatches 21; Indels 1; Gaps 1;

Qy 2 TVALGSPAGPAELSLRLGPEPLTYS-EDGDMWTYLSVSGSENNISVAV 54
 Db 79 TFLVYKDKRKEDLSFYKSGENLIQITISKODGMLRLSLRTGEGYIPSNYIA 132

RESULT 14
 ID Q8WQMS PRELIMINARY; PRT; 511 AA.
 AC Q8WQMS.
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Src-family protein tyrosine kinase.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinzoa;
 OC Strongylocentrotus; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 NX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Giusti A.F., O'Neill F.J., Yamae K., Foltz K.R., Jaffe L.A.;
 RT "Function of a sea urchin egg src-family kinase in initiating Ca2+ release at fertilization."
 RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY063749; ARL50111.1;
 DR InterPro: IPR0000719; Euk_pkinase.
 DR InterPro: IPR002280; Ser_thr_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TykC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; UNKNOWN; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW KINASE.
 SO SEQUENCE 511 AA; 57726 MW; D3856B7B0D46716D CRC64;

Query Match 32.3%; Score 93; DB 5; Length 511;
 Best Local Similarity 36.5%; Pred. No. 0.0065;
 Matches 19; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

Qy 5 ALGSPAGPAELSLRLGPEPLTYS-EDGDMWTYLSVSGSENNISVAV 56
 Db 67 ALYDYDAESDDDDPKKKGLLVVTETEDMWLRSGTKKEGYIPSNVAVP 118

RESULT 15
 ID Q9V9J3 PRELIMINARY; PRT; 517 AA.
 AC Q9V9J3; Q94879; Q18369; Q26297;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Tyrosine-protein kinase Src42A (EC 2.7.1.112).
 GN SRC42A OR SRC41 OR IK5 OR CG7873.
 OS Drosophila melanogaster (Fruit Fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Archopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
 RC STRAIN=CANTON-S; TISSUE=PUPAE;
 RX MEDLINE=96268448; PubMed=8682295;
 RA Takahashi F., Endo S., Kojima T., Saigo K.;
 RT "Regulation of cell-cell contacts in developing Drosophila eyes by Dsrc4, a new, close relative of vertebrate c-src."
 RL Genes Dev. 10:1645-1656(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Georges R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer V., Chapple M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-U., Andrews-Frankoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bokkova D., Botchan M.R., Bouck J., Brooks P., Brattler P.,
 RA Buttle K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferrar C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K.,
 RA Glöckner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris B.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mates B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Modary C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY; TISSUE=EMBRYO;
 RA Stapleton M., Brokslein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Fisse E., George R.,
 RA Gonzalez M., Garin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunco J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE OF 374-428 FROM N.A.
 RX MEDLINE=92008631; PubMed=1915852;
 RA Shihido E., Emori Y., Saigo K.;
 RT "Identification of seven novel protein-tyrosine kinase genes of
 RL Drosophila by the polymerase chain reaction.";
 RN FEBS Lett. 289:235-238(1991).
 RP SEQUENCE OF 376-427 FROM N.A.
 RC TISSUE=EMBRYO;
 RX MEDLINE=98401146; PubMed=9711193;
 RA Oates A.C., Wolberg P., Achen M.G., Wilks A.F.;
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT polymerase chain reaction with genomic DNA.";
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
 CC -1- FUNCTION: ESSENTIAL FOR CORRECT EYE MORPHOGENESIS (OMMATIDIAL R7
 CC NEURON FORMATION), THIS REQUIRES THE RAS1/MAK SIGNAL TRANSDUCTION
 CC ORGANIZATION AND CELL-CELL CONTACTS IN DEVELOPING OMMATIDIA.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS IN EARLY EMBRYOS, IN STAGES 13-16
 CC EXPRESSION IS SEEN IN VISCERAL MESODERM, HINDGUT, BRAIN, ANAL PADS
 CC AND VENTRAL GANGLIONS. IN LARVAE, EXPRESSION IS IN CNS, WING DISK,
 CC LEG DISK AND PHOTORECEPTOR PRECURSORS IN THE EYE-ANTENNA DISKS
 CC POSTERIOR TO THE MORPHOGENETIC FURROW.
 CC -1- DEVELOPMENTAL STAGE: IN EARLY EMBRYOS EXPRESSION IS VERY LOW,
 CC EXPRESSION INCREASES DURING EMBRYOGENESIS. ALSO EXPRESSED IN
 CC LARVAE AND PUPAE.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 DR EMBL: D42125; BAA07705.1; -;
 DR EMBL: AE003784; AAF57295.1; -;
 DR EMBL: AY058652; AAL13881.1; -;
 DR EMBL: S55977; AAB19907.1; -;
 DR EMBL: AJ002911; CA05746.1; -;
 DR HSSP: P00523; ISRL.
 DR Flybase: FBgn0004603; Src42A.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0452; SH3DOMAIN.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TIR; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW transferase; kinase; Tyrosine-protein kinase; ATP-binding; SH2 domain;
 KW SH3 domain; developmental protein.
 FT DOMAIN 63 124 SH3.
 FT DOMAIN 130 222 SH2.
 FT DOMAIN 248 504 PROTEIN_KINASE.
 FT NP_BIND 254 262 ATP (BY SIMILARITY).
 FT BINDING 276 276 ATP (BY SIMILARITY).
 FT ACT_SITE 370 370 BY SIMILARITY.
 FT CONFLICT 65 65 A -> V (IN REF. 1).
 FT CONFLICT 376 376 V -> I (IN REF. 4 AND 5).
 FT CONFLICT 381 386 GN1YKI -> SNVYGM (IN REF. 4).

SO SEQUENCE 517 AA; 59069 MW; 1EF196E4D7AE61E9 CRC64;
 Query Match 31.8%; Score 91.5; DB 5; Length 517;
 Best Local Similarity 42.6%; Pred. No. 0.01;
 Matches 23; Conservative 9; Mismatches 21; Indels 1; Gaps 1;
 Oy 4 VALGSPAGGPAELISRLGELPTIVSE-DDDWMTVLSEVSGREYNIPSHVAVKY 56
 Db 69 VALYDARDTDEDLSFRKGHELEILINDQGDWWLARSKTSSEGYIPSNVAVLT 122
 Search completed: March 24, 2003, 15:50:35
 Job time : 10.4182 secs

